



US 20210317525A1

(19) **United States**(12) **Patent Application Publication**
BIELAS(10) **Pub. No.: US 2021/0317525 A1**(43) **Pub. Date: Oct. 14, 2021**(54) **COMPOSITIONS AND METHODS FOR
ACCURATELY IDENTIFYING MUTATIONS**(71) Applicant: **Fred Hutchinson Cancer Research
Center, Seattle, WA (US)**(72) Inventor: **Jason H. BIELAS, Seattle, WA (US)**(21) Appl. No.: **17/356,288**(22) Filed: **Jun. 23, 2021****Related U.S. Application Data**

(60) Continuation of application No. 17/219,543, filed on Mar. 31, 2021, which is a continuation of application No. 16/898,155, filed on Jun. 10, 2020, now abandoned, which is a continuation of application No. 16/657,898, filed on Oct. 18, 2019, now abandoned, which is a continuation of application No. 16/121,559, filed on Sep. 4, 2018, now abandoned, which is a continuation of application No. 15/199,784, filed on Jun. 30, 2016, now Pat. No. 10,450,606, which is a division of application No. 14/378,870, filed on Aug. 14, 2014, now Pat. No. 10,011,871, filed as application No. PCT/US2013/026505 on Feb. 15, 2013.

(60) Provisional application No. 61/600,535, filed on Feb. 17, 2012.

Publication Classification(51) **Int. Cl.**

<i>C12Q 1/6874</i>	(2006.01)
<i>C40B 40/08</i>	(2006.01)
<i>C40B 50/06</i>	(2006.01)
<i>C12N 15/10</i>	(2006.01)
<i>C12Q 1/6827</i>	(2006.01)
<i>C12N 15/81</i>	(2006.01)
<i>C12N 15/85</i>	(2006.01)
<i>C12N 15/70</i>	(2006.01)
<i>C12Q 1/6869</i>	(2006.01)

(52) **U.S. Cl.**

CPC *C12Q 1/6874* (2013.01); *C40B 40/08* (2013.01); *C40B 50/06* (2013.01); *C12N 15/10* (2013.01); *C12Q 1/6827* (2013.01); *C12Q 1/6869* (2013.01); *C12N 15/85* (2013.01); *C12N 15/1093* (2013.01); *C12N 15/1065* (2013.01); *C12N 15/70* (2013.01); *C12N 15/81* (2013.01)

(57)

ABSTRACT

The present disclosure provides compositions and methods for accurately detecting mutations by uniquely tagging double stranded nucleic acid molecules with dual cyphers such that sequence data obtained from a sense strand can be linked to sequence data obtained from an anti-sense strand when sequenced, for example, by massively parallel sequencing methods.

Specification includes a Sequence Listing.